Supplementary Table S2. Genes upregulated under iron-replete growth

Rv no.	Gene name	B	Fold change	Putative function
☆Rv0001	dnaA	0.59	0.38	CHROMOSOMAL REPLICATION INITIATOR PROTEIN
Rv0007		3.24	0.33	CONSERVED MEMBRANE PROTEIN
Rv0011c		4.84	0.23	CONSERVED MEMBRANE PROTEIN
Rv0022c		1.62	0.19	TRANSCRIPTIONAL REGULATORY PROTEIN WHIB-LIKE WHIB5
Rv0025		0.28	0.43	CONSERVED HYPOTHETICAL PROTEIN
Rv0027		0.88	0.22	CONSERVED HYPOTHETICAL PROTEIN
Rv0028		3.40	0.12	CONSERVED HYPOTHETICAL PROTEIN
Rv0030		1.10	0.31	CONSERVED HYPOTHETICAL PROTEIN
Rv0031		1.88	0.23	REMNANT OF A TRANSPOSASE
Rv0033		7.89	0.08	ACYL CARRIER PROTEIN ACPA (ACP)
Rv0053	rpsF	5.22	0.27	30S RIBOSOMAL PROTEIN S6 RPSF
Rv0055	rpsR	4.33	0.23	30S RIBOSOMAL PROTEIN S18-1 RPSR1
Rv0060		1.04	0.01	CONSERVED HYPOTHETICAL PROTEIN
Rv0067c		4.87	0.18	TRANSCRIPTIONAL REGULATORY PROTEIN (TETR-FAMILY)
Rv0072		6.95	0.13	GLUTAMINE-TRANSPORT TRANSMEMBRANE PROTEIN
Rv0077c		2.16	0.42	OXIDOREDUCTASE
Rv0081		1.44	0.10	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0088		0.38	0.49	HYPOTHETICAL PROTEIN
Rv0091		1.07	0.43	BIFUNCTIONAL MTA/SAH NUCLEOSIDASE
Rv0095c		3.534	0.18	CONSERVED HYPOTHETICAL PROTEIN
Rv0166	fadD5.	0.94	0.28	FATTY-ACID-COA LIGASE FADD5
Rv0167		3.53	0.25	INTEGRAL MEMBRANE PROTEIN YRBE1A
Rv0168		2.75	0.30	INTEGRAL MEMBRANE PROTEIN YRBE1B
Rv0169	mce1.	0.39	0.48	MCE-FAMILY PROTEIN MCE1A
Rv0171		3.86	0.33	MCE-FAMILY PROTEIN MCE1C

Rv0173	lprK.	0.45	0.50	MCE-FAMILY LIPOPROTEIN LPRK
Rv0179c	lprO.	2.53	0.28	LIPOPROTEIN LPRO
✪Rv0250c		2.56	0.35	CONSERVED HYPOTHETICAL PROTEIN
Rv0256c		0.58	0.46	PPE
Rv0257c		2.38	0.37	CONSERVED HYPOTHETICAL PROTEIN
Rv0273c		3.43	0.29	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0280	PPE	1.65	0.24	PPE
Rv0297	PE. PGRS	1.84	0.47	PE.PGRS
Rv0298		4.56	0.33	HYPOTHETICAL PROTEIN
Rv0302		0.21	0.53	TRANSCRIPTIONAL REGULATORY PROTEIN (TETR/ACRR-FAMILY)
Rv0322	udgA.	4.08	0.24	PROBABLE UDP-GLUCOSE 6-DEHYDROGENASE UDGA
Rv0324		1.91	0.39	TRANSCRIPTIONAL REGULATORY PROTEIN (ARSR-FAMILY)
Rv0360c		2.93	0.24	CONSERVED HYPOTHETICAL PROTEIN
Rv0366c		3.96	0.18	CONSERVED HYPOTHETICAL PROTEIN
Rv0369c		1.95	0.42	MEMBRANE OXIDOREDUCTASE
Rv0403c	mmpS1.	0.38	0.45	CONSERVED MEMBRANE PROTEIN MMPS1
Rv0404	fadD30.	3.99	0.24	FATTY-ACID-COA LIGASE FADD30 (FATTY-ACID-COA SYNTHETASE
✪Rv0430		6.30	0.22	CONSERVED HYPOTHETICAL PROTEIN
Rv0431		2.85	0.40	TUBERCULIN RELATED PEPTIDE
Rv0435c		1.33	0.21	CONSERVED ATPASE
Rv0443		1.54	0.42	CONSERVED HYPOTHETICAL PROTEIN
Rv0460		1.06	0.41	CONSERVED HYDROPHOBIC PROTEIN
☆Rv0463		0.69	0.50	CONSERVED MEMBRANE PROTEIN
Rv0477		4.09	0.26	CONSERVED SECRETED PROTEIN
Rv0506	mmpS2.	3.43	0.41	CONSERVED MEMBRANE PROTEIN MMPS2
Rv0544c		5.19	0.28	CONSERVED TRANSMEMBRANE PROTEIN
Rv0565c		0.45	0.51	MONOOXYGENASE

Rv0581		2.39	0.38	CONSERVED HYPOTHETICAL PROTEIN
Rv0602c	tcrA.	2.27	0.27	TWO COMPONENT DNA BINDING TRANSCRIPTIONAL REGULATOR
Rv0604	lpqO.	2.36	0.43	CONSERVED LIPOPROTEIN LPQO
Rv0625c		0.57	0.36	CONSERVED TRANSMEMBRANE PROTEIN
Rv0651	rplJ.	1.57	0.47	50S RIBOSOMAL PROTEIN L10 RPLJ
Rv0661c		0.67	0.39	CONSERVED HYPOTHETICAL PROTEIN
Rv0662c		1.03	0.47	CONSERVED HYPOTHETICAL PROTEIN
Rv0683	rpsG.	1.03	0.42	30S RIBOSOMAL PROTEIN S7 RPSG
Rv0689c		4.00	0.29	HYPOTHETICAL PROTEIN
Rv0690c		0.57	0.52	CONSERVED HYPOTHETICAL PROTEIN
Rv0698		4.54	0.19	CONSERVED HYPOTHETICAL PROTEIN
Rv0699		2.22	0.19	HYPOTHETICAL PROTEIN
Rv0702	rplD.	1.86	0.48	50S RIBOSOMAL PROTEIN L4 RPLD
Rv0705	rpsS.	2.58	0.44	30S RIBOSOMAL PROTEIN S19 RPSS
Rv0724	sppA.	1.23	0.40	POSSIBLE PROTEASE IV SPPA
Rv0731c		2.68	0.35	CONSERVED HYPOTHETICAL PROTEIN
Rv0739		1.85	0.19	CONSERVED HYPOTHETICAL PROTEIN
Rv0742	PE. PGRS	2.18	0.34	PE.PGRS
Rv0743c		4.45	0.35	HYPOTHETICAL PROTEIN
Rv0748		3.59	0.30	CONSERVED HYPOTHETICAL PROTEIN
Rv0750		0.12	0.52	CONSERVED HYPOTHETICAL PROTEIN
Rv0759c		4.87	0.37	CONSERVED HYPOTHETICAL PROTEIN
Rv0762c		0.23	0.46	CONSERVED HYPOTHETICAL PROTEIN
Rv0763c		0.30	0.45	FERREDOXIN
Rv0767c		0.74	0.44	CONSERVED HYPOTHETICAL PROTEIN
Rv0781	ptrBb.	3.12	0.34	PROTEASE II PTRBA
Rv0793		0.9	0.32	CONSERVED HYPOTHETICAL PROTEIN

Rv0800	pepC.	1.64	0.46	AMINOPEPTIDASE PEPC
Rv0801		0.45	0.42	CONSERVED HYPOTHETICAL PROTEIN
Rv0829		2.16	0.45	TRANSPOSASE (FRAGMENT)
✰Rv0878c	PPE	1.45	0.43	PPE
Rv0879c		1.97	0.36	CONSERVED TRANSMEMBRANE PROTEIN
Rv0893c		0.33	0.48	CONSERVED HYPOTHETICAL PROTEIN
Rv0903c	prrA	1.85	0.03	TWO COMPONENT RESPONSE TRANSCRIPTIONAL REGULATOR
Rv0927c		3.03	0.30	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
Rv0947c		0.93	0.32	MYCOLYL TRANSFERASE
Rv0957	purH.	0.05	0.50	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH
Rv0977	PE	0.56	0.42	PE
Rv0979c		3.46	0.37	50S RIBOSOMAL PROTEIN L32 RPMF
Rv0992c		0.53	0.36	CONSERVED HYPOTHETICAL PROTEIN
Rv1012		2.46	0.30	HYPOTHETICAL PROTEIN
Rv1040c	PE	3.65	0.31	PE
Rv1053c		1.92	0.46	HYPOTHETICAL PROTEIN
Rv1083		2.11	0.33	CONSERVED HYPOTHETICAL PROTEIN
Rv1089	PE	4.59	0.10	PE
Rv1103c		0.22	0.53	CONSERVED HYPOTHETICAL PROTEIN
Rv1105		0.11	0.28	PARA-NITROBENZYL ESTERASE
Rv1107c	xseB.	0.42	0.50	EXODEOXYRIBONUCLEASE VII (SMALL SUBUNIT) XSEA
Rv1119c		1.26	0.29	HYPOTHETICAL PROTEIN
Rv1124	ephC.	1.34	0.39	EPOXIDE HYDROLASE EPHC
Rv1135c	PPE	5.89	0.18	PPE
Rv1154c		2.79	0.42	HYPOTHETICAL PROTEIN
Rv1172c	PE	4.23	0.22	PE
Rv1230c		3.65	0.36	MEMBRANE PROTEIN

Rv1241		0.13	0.53	CONSERVED HYPOTHETICAL PROTEIN
Rv1261c		0.35	0.57	CONSERVED HYPOTHETICAL PROTEIN
Rv1271c		1.13	0.36	CONSERVED HYPOTHETICAL SECRETED PROTEIN
✪Rv1305	atpE.	0.46	0.52	ATP SYNTHASE C CHAIN ATPE (LIPID-BINDING PROTEIN)
Rv1320c		2.42	0.45	ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE
Rv1363c		1.91	0.42	MEMBRANE PROTEIN
Rv1365c		1.30	0.33	ANTI-ANTI-SIGMA FACTOR RSFA
Rv1372	pks18	1.57	0.34	CONSERVED HYPOTHETICAL PROTEIN
RV1386	PE	3.88	0.31	PE
Rv1403c		0.81	0.28	METHYLTRANSFERASE
Rv1423		0.32	0.45	TRANSCRIPTIONAL REGULATORY PROTEIN WHIA
Rv1426c	lipO	1.87	0.43	ESTERASE LIPO
Rv1430	PE	0.57	0.44	PE
Rv1453		0.79	0.03	TRANSCRIPTIONAL ACTIVATOR PROTEIN
Rv1470	trxA	0.05	0.34	THIOREDOXIN TRXA
Rv1506c		6.30	0.20	HYPOTHETICAL PROTEIN
Rv1507c		1.08	0.44	CONSERVED HYPOTHETICAL PROTEIN
Rv1549	fadD11	1.04	0.36	FATTY-ACID-COA LIGASE FADD11
Rv1550	fadD11	5.60	0.18	FATTY-ACID-COA LIGASE FADD11
Rv1555	frdD	8.46	0.09	FUMARATE REDUCTASE
Rv1580c		2.20	0.43	PROBABLE PHIRV1 PHAGE PROTEIN
Rv1581c		2.13	0.44	PROBABLE PHIRV1 PHAGE PROTEIN
Rv1622c	cydB	3.89	0.01	INTEGRAL MEMBRANE CYTOCHROME D UBIQUINOL OXIDASE
Rv1642	rpmI.	1.06	0.42	50S RIBOSOMAL PROTEIN L35 RPMI
Rv1645c		3.29	0.32	CONSERVED HYPOTHETICAL PROTEIN
Rv1660	pks10.	0.88	0.50	CHALCONE SYNTHASE PKS10
Rv1665	pks11.	7.01	0.21	CHALCONE SYNTHASE PKS11

Rv1705c	PPE	4.66	0.21	PPE
Rv1729c		1.13	0.37	CONSERVED HYPOTHETICAL PROTEIN
Rv1759	PE. PGRS	0.55	0.43	PE.PGRS
Rv1766		2.03	0.43	CONSERVED HYPOTHETICAL PROTEIN
Rv1790	PPE	0.33	0.54	PPE
Rv1801	PPE	1.25	0.43	PPE
Rv1851	ureF	4.08	0.40	UREASE ACCESSORY PROTEIN UREF
Rv1802	PPE	2.03	0.35	PPE
Rv1860	modD	3.43	0.38	ALANINE AND PROLINE RICH SECRETED PROTEIN APA
☆Rv1871c		0.25	0.58	CONSERVED HYPOTHETICAL PROTEIN
✪Rv1876	bfrA	4.94	0.21	BACTERIOFERRITIN BFRA
Rv1884c		4.29	0.27	RESUSCITATION-PROMOTING FACTOR RPFC
Rv1893		0.23	0.49	CONSERVED HYPOTHETICAL PROTEIN
Rv1909c	furA	0.54	0.54	FERRIC UPTAKE REGULATION PROTEIN FURA (FUR)
Rv1916	aceAb	1.02	0.48	ISOCITRATE LYASE ACEAB [SECOND PART]
✪Rv1943c		0.44	0.54	CONSERVED HYPOTHETICAL PROTEIN
Rv1952		4.09	0.21	CONSERVED HYPOTHETICAL PROTEIN
Rv1957		4.19	0.24	HYPOTHETICAL PROTEIN
Rv1961		3.71	0.31	HYPOTHETICAL PROTEIN
Rv1962c		1.18	0.53	CONSERVED HYPOTHETICAL PROTEIN
Rv1972		1.58	0.39	CONSERVED MCE ASSOCIATED MEMBRANE PROTEIN
Rv1981c	nrdF	0.79	0.33	CONSERVED HYPOTHETICAL PROTEIN
Rv2020c		5.23	0.32	CONSERVED HYPOTHETICAL PROTEIN
Rv2055c	rpsR2	0.77	0.29	RIBOSOMAL PROTEIN S18 RPSR2
Rv2060		2.62	0.24	CONSERVED INTEGRAL MEMBRANE PROTEIN
Rv2063c		2.33	0.35	CONSERVED HYPOTHETICAL PROTEIN
Rv2083		0.12	0.48	CONSERVED HYPOTHETICAL PROTEIN

Rv2085		0.22	0.34	CONSERVED HYPOTHETICAL PROTEIN
Rv2111c		4.76	0.23	CONSERVED HYPOTHETICAL PROTEIN
Rv2127	ansP	3.83	0.36	L-ASPARAGINE PERMEASE ANSP1
Rv2128		2.21	0.39	CONSERVED TRANSMEMBRANE PROTEIN
Rv2186c		0.84	0.52	CONSERVED HYPOTHETICAL PROTEIN
Rv2197c		2.79	0.41	CONSERVED TRANSMEMBRANE PROTEIN
Rv2198c	mmpS3	0.11	0.34	CONSERVED MEMBRANE PROTEIN MMPS3
Rv2223c		1.55	0.41	EXPORTED PROTEASE
Rv2232		1.89	0.41	CONSERVED HYPOTHETICAL PROTEIN
Rv2237		0.74	0.53	CONSERVED HYPOTHETICAL PROTEIN
Rv2242		2.72	0.38	CONSERVED HYPOTHETICAL PROTEIN
Rv2249c	glpD1	5.81	0.19	GLYCEROL-3-PHOSPHATE DEHYDROGENASE GLPD1
Rv2270	lppN	5.04	0.26	LIPOPROTEIN LPPN
Rv2274c		4.64	0.19	HYPOTHETICAL PROTEIN
Rv2284	lipM	0.48	0.53	ESTERASE LIPM
Rv2288		2.78	0.28	HYPOTHETICAL PROTEIN
Rv2292c		6.52	0.21	HYPOTHETICAL PROTEIN
Rv2295		3.52	0.39	CONSERVED HYPOTHETICAL PROTEIN
Rv2304c		0.13	0.44	HYPOTHETICAL PROTEIN
Rv2311		4.68	0.23	CONSERVED HYPOTHETICAL PROTEIN
Rv2331		0.09	0.50	HYPOTHETICAL PROTEIN
Rv2338c	moeW	0.40	0.59	MOLYBDOPTERIN BIOSYNTHESIS PROTEIN MOEW
Rv2339	mmpL9	4.04	0.34	CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL9
Rv2341	LppQ	2.87	0.18	CONSERVED LIPOPROTEIN LPPQ
Rv2342		1.16	0.52	CONSERVED HYPOTHETICAL PROTEIN
Rv2349c	plcC	0.24	0.46	PHOSPHOLIPASE C 3 PLCC
Rv2350c	plcB	0.74	0.36	MEMBRANE-ASSOCIATED PHOSPHOLIPASE C 2 PLCB

Rv2356c	PPE	2.86	0.36	PPE
Rv2396c	PE PGRS	1.04	0.50	PE.PGRS
Rv2399c	cysT	1.83	0.52	SULFATE-TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER CYST
Rv2401		0.13	0.38	CONSERVED MEMBRANE PROTEIN
Rv2406c		5.49	0.34	CONSERVED HYPOTHETICAL PROTEIN
Rv2416c		0.59	0.53	ENHANCED INTRACELLULAR SURVIVAL PROTEIN EIS
Rv2418c		1.24	0.31	HYPOTHETICAL PROTEIN
Rv2741	PE. PGRS	3.64	0.46	PE.PGRS
Rv2472		3.24	0.40	CONSERVED HYPOTHETICAL PROTEIN
Rv2485c	lipQ	2.82	0.24	CARBOXYLESTERASE LIPQ
Rv2493		2.93	0.45	CITRATE (PRO-3S)-LYASE (BETA SUBUNIT) CITE
Rv2517c		5.68	0.40	HYPOTHETICAL PROTEIN
✪Rv2526		2.94	0.23	HYPOTHETICAL PROTEIN
Rv2529		0.79	0.47	HYPOTHETICAL PROTEIN
Rv2537c	aroD	0.47	0.53	3-DEHYDROQUINATE DEHYDRATASE AROD
Rv2547		3.04	0.38	CONSERVED HYPOTHETICAL PROTEIN
✪Rv2549c		0.81	0.36	CONSERVED HYPOTHETICAL PROTEIN
Rv2560		0.06	0.50	PROLINE AND GLYCINE RICH TRANSMEMBRANE PROTEIN
Rv2561		4.07	0.44	CONSERVED HYPOTHETICAL PROTEIN
Rv2562		3.59	0.41	CONSERVED HYPOTHETICAL PROTEIN
Rv2564	glnQ	1.09	0.34	GLUTAMINE-TRANSPORT ATP-BINDING PROTEIN
Rv2599		1.07	0.39	CONSERVED MEMBRANE PROTEIN
Rv2600		3.78	0.29	CONSERVED INTEGRAL MEMBRANE PROTEIN
Rv2608	PPE	1.07	0.36	PPE
Rv2615c	PE.PGRS	0.80	0.47	PE.PGRS
Rv2632c		2.84	0.43	CONSERVED HYPOTHETICAL PROTEIN
Rv2640c		3.96	0.15	TRANSCRIPTIONAL REGULATORY PROTEIN (ARSR-FAMILY)

Rv2645		5.41	0.15	HYPOTHETICAL PROTEIN
Rv2653c		0.81	0.35	PHIRV2 PROPHAGE PROTEIN
Rv2657c		1.31	0.45	PHIRV2 PROPHAGE PROTEIN
Rv2658c		2.47	0.44	PROPHAGE PROTEIN
Rv2664		2.08	0.42	HYPOTHETICAL PROTEIN
Rv2665		4.26	0.35	HYPOTHETICAL ARGININE RICH PROTEIN
Rv2669		0.83	0.27	HYPOTHETICAL PROTEIN
Rv2687c		1.73	0.28	INTEGRAL MEMBRANE LEUCINE AND VALINE RICH PROTEIN
Rv2691	trkA	3.13	0.48	TRK SYSTEM POTASSIUM UPTAKE PROTEIN CEOB
Rv2717c		1.28	0.38	CONSERVED HYPOTHETICAL PROTEIN
Rv2760c		4.32	0.13	CONSERVED HYPOTHETICAL PROTEIN
Rv2762c		1.50	0.43	CONSERVED HYPOTHETICAL PROTEIN
Rv2781c		0.53	0.53	ALANINE RICH OXIDOREDUCTASE
Rv2785c	rpsO	0.69	0.52	30S RIBOSOMAL PROTEIN S15 RPSO
Rv2804c		0.35	0.41	HYPOTHETICAL PROTEIN
☆Rv2816c		1.94	0.42	CONSERVED HYPOTHETICAL PROTEIN
Rv2820c		2.26	0.46	HYPOTHETICAL ARGININE AND ALANINE RICH PROTEIN
Rv2910c		0.16	0.41	CONSERVED HYPOTHETICAL PROTEIN
Rv2952		1.79	0.42	METHYLTRANSFERASE (METHYLASE
Rv2960c		4.47	0.33	HYPOTHETICAL PROTEIN
Rv2962c		1.90	0.47	GLYCOSYL TRANSFERASE
Rv2965c	kdtB	1.17	0.32	PHOSPHOPANTETHEINE ADENYLYLTRANSFERASE KDTB
Rv2997		1.58	0.41	ALANINE RICH DEHYDROGENASE
Rv3007c		2.02	0.47	OXIDOREDUCTASE
Rv3012c	gatC	0.59	0.53	GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE (SUBUNIT C) GATC
Rv3015c		1.09	0.33	CONSERVED HYPOTHETICAL PROTEIN
Rv3017c		1.12	0.47	ESAT-6 LIKE PROTEIN ESXQ

Rv3033		0.09	0.51	HYPOTHETICAL PROTEIN
Rv3036c		0.70	0.46	CONSERVED SECRETED PROTEIN TB22.2
Rv3063	cstA	2.49	0.47	CARBON STARVATION PROTEIN A HOMOLOG CSTA
Rv3065	emrE	1.48	0.39	MULTIDRUGS-TRANSPORT INTEGRAL MEMBRANE PROTEIN MMR
Rv3067		1.78	0.45	CONSERVED HYPOTHETICAL PROTEIN
Rv3076		1.18	0.48	CONSERVED HYPOTHETICAL PROTEIN
Rv3085		0.65	0.19	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
Rv3088		1.58	0.43	CONSERVED HYPOTHETICAL PROTEIN
Rv3093c		1.82	0.54	HYPOTHETICAL OXIDOREDUCTASE
Rv3018c		0.32	0.43	PPE
Rv3106	fprA	0.18	0.49	NADPH:ADRENODOXIN OXIDOREDUCTASE FPRA
Rv3110	moaB	6.08	0.15	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE MOAB1
Rv3119	moaE	0.08	0.46	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN E MOAE1
Rv3125c	PPE	2.16	0.45	PPE
Rv3142c		2.62	0.42	HYPOTHETICAL PROTEIN
Rv3143		3.18	0.32	RESPONSE REGULATOR
✪Rv3147	nuoC	0.20	0.51	NADH DEHYDROGENASE I
Rv3151	nuoG	0.40	0.39	NADH DEHYDROGENASE I (CHAIN G) NUOG
✪Rv3155	nuoK	0.74	0.31	NADH DEHYDROGENASE I (CHAIN K) NUOK
Rv3165c		3.03	0.37	HYPOTHETICAL PROTEIN
Rv3178		4.33	0.19	CONSERVED HYPOTHETICAL PROTEIN
Rv3183		0.48	0.34	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv3222c		0.12	0.50	CONSERVED HYPOTHETICAL PROTEIN
Rv3243c		1.52	0.47	HYPOTHETICAL PROTEIN
Rv3280	accD5	0.81	0.48	PROPIONYL-COA CARBOXYLASE BETA CHAIN 5 ACCD5
Rv3317	sdhD	1.68	0.53	SUCCINATE DEHYDROGENASE
✪Rv3320c		4.66	0.32	CONSERVED HYPOTHETICAL PROTEIN

Rv3323c	gphA	1.03	0.36	MOAD-MOAE FUSION PROTEIN MOAX
Rv3345c	PE. PGRS	0.43	0.34	PE.PGRS
☆Rv3346c		1.51	0.37	CONSERVED TRANSMEMBRANE PROTEIN
Rv3353c		3.24	0.35	CONSERVED HYPOTHETICAL PROTEIN
☆Rv3354		3.67	0.41	CONSERVED HYPOTHETICAL PROTEIN
Rv3386		3.0751	0.42	TRANSPOSASE
Rv3392c	cmaA1	0.68	0.42	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1
Rv3444c		0.03	0.39	ESAT-6 LIKE PROTEIN ESXT
Rv3494c		1.46	0.43	MCE-FAMILY PROTEIN MCE4F
Rv3497c		0.71	0.42	MCE-FAMILY PROTEIN MCE4F
Rv3511	PE. PGRS	0.54	0.52	PE.PGRS
Rv3512	PE. PGRS	0.53	0.26	PE.PGRS
Rv3558	PPE	3.48	0.34	PPE
☆Rv3612c		3.19	0.43	CONSERVED HYPOTHETICAL PROTEIN
☆Rv3613c		8.59	0.13	HYPOTHETICAL PROTEIN
Rv3622c		1.06	0.26	PE
Rv3640c		0.94	0.29	TRANSPOSASE
Rv3642c		0.70	0.44	HYPOTHETICAL PROTEIN
Rv3746c		2.32	0.34	PE
Rv3648c	cspA	7.27	0.34	COLD SHOCK PROTEIN A CSPA
Rv3687c		4.06	0.18	ANTI-ANTI-SIGMA FACTOR RSFB
Rv3688c		1.53	0.36	CONSERVED HYPOTHETICAL PROTEIN
Rv3702c		3.12	0.13	CONSERVED HYPOTHETICAL PROTEIN
Rv3716c		0.60	0.30	CONSERVED HYPOTHETICAL PROTEIN
Rv3724		0.51	0.54	CUTINASE CUT5B
Rv3729		0.28	0.32	TRANSFERASE
Rv3738c		2.47	0.51	PPE

Rv3744		2.38	0.43	TRANSCRIPTIONAL REGULATORY PROTEIN (ARSR-FAMILY)
Rv3750c		0.74	0.53	EXCISIONASE
Rv3752c		0.93	0.40	CYTIDINE/DEOXYCYTIDYLATE DEAMINASE
Rv3760		1.53	0.45	CONSERVED MEMBRANE PROTEIN
Rv3786c		3.80	0.04	HYPOTHETICAL PROTEIN
Rv3816c		1.29	0.48	ACYLTRANSFERASE
✪Rv3841	bfrB	0.79	0.19	BACTERIOFERRITIN BFRB
Rv3851		1.02	0.51	MEMBRANE PROTEIN
Rv3857c		0.47	0.51	MEMBRANE PROTEIN

✪Genes found to be repressed in *M. tuberculosis* (H37Rv) under low-iron conditions by Rodriguez et al. (2002).
✰Genes found to be upregulated in *M. tuberculosis* (H37Rv) under low-iron conditions by Rodriguez et al. (2002).